



- ▶ As always, we have three stages in mind:
 - ▶ Monitoring residuals during alignment algorithm: `CommonAlignmentMonitor` (10,000 histograms)
 - ▶ Monitoring tracks and residuals in a test re-reconstruction after alignment: `MuonAlignmentAnalyzer` → DQM (500-700 histograms)
 - ▶ Comparison of geometries at the database level (undefined)
- ▶ `CommonAlignmentMonitor`: it was supposed to manage histogram merging with iterations, but almost all HIP procedures need to parallelize, so we can't iterate in the same directory anyway. So the only useful thing it does is merge histograms after parallelization, but there are ROOT errors when it tries to do that!

As far as I know, everyone merges the histograms outside of `CommonAlignmentMonitor`, not using the collector mechanism. Not a show-stopper, but it's not working as intended. I haven't decided what to do about that.
- ▶ `MuonAlignmentAnalyzer`: Pablo talked about that
- ▶ Database comparison: a lot of infrastructure development finished this week— I hope to upload later today.